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RAW SEQUENCE LISTING

DATE: 03/26/2002

PATENT APPLICATION: US/10/092,135

TIME: 12:33:42

Input Set : A:\EP.txt

Output Set: N:\CRF3\03262002\J092135.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company
 5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED
 RECEPTOR,

6 HGPRBMY27

8 <130> FILE REFERENCE: D0134.NP

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/092,135

C--> 10 <141> CURRENT FILING DATE: 2002-03-06

10 <150> PRIOR APPLICATION NUMBER: US 60/273,808

11 <151> PRIOR FILING DATE: 2001-03-07

13 <150> PRIOR APPLICATION NUMBER: US 60/278,983

14 <151> PRIOR FILING DATE: 2001-03-27

16 <160> NUMBER OF SEQ ID NOS: 75

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 2580

22 <212> TYPE: DNA

23 <213> ORGANISM: homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (457)..(1482)

29 <400> SEQUENCE: 1

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30 ccaataacaa ccggggcggtt caccttcgga tttagcaagg ttttgaaaaa ctatttaggt      60
32 gcccataaaa ggtcccttc aggtaccggt ccgaaattcc gggtaacccc aggggtccgga      120
34 tcaattaagg gtctgggggg tggccacctg gccactttgg aaaattgcaa gcatttccaa      180
36 gcttcacccg gctccagggt tggcctctcc aaaaggcagg cggcttttaa acgggttcca      240
38 acagaaagga cctcccttgg tctcctcaat tcctggctgg agtttctctt ctctgtgtgt      300
40 ggaaggattc caaaccacac cacacaggac ccgcatactg ggtgatgaag tcagacacgc      360
42 agcagctggg tgagtgtctac gctcaagata agcatctgtg ccattgtggg gactccctgg      420
44 gctgctctgc acccggtacac ttgctctgtc cccgcc atg tac aac ggg tgc tgc      474
45                                     Met Tyr Asn Gly Ser Cys
46                                     1           5
48 tgc cgc atc gag ggg gac acc atc tcc cag gtg atg ccg ccg ctg ctg      522
49 Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln Val Met Pro Pro Leu Leu
50      10           15           20
52 att gtg gcc ttt gtg ctg ggc gca cta ggc aat ggg gtc gcc ctg tgt      570
53 Ile Val Ala Phe Val Leu Gly Ala Leu Gly Asn Gly Val Ala Leu Cys
54      25           30           35
56 ggt ttc tgc ttc cac atg aag acc tgg aag ccc agc act gtt tac ctt      618
57 Gly Phe Cys Phe His Met Lys Thr Trp Lys Pro Ser Thr Val Tyr Leu
58      40           45           50

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65 Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly Asp Ile
66          75          80          85
68 ccc tgc cga gtg ggg ctc ttc acg ttg gcc atg aac agg gcc ggg agc      762
69 Pro Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala Gly Ser
70          90          95          100
72 atc gtg ttc ctt acg gtg gtg gct gcg gac agg tat ttc aaa gtg gtc      810
73 Ile Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys Val Val
74          105          110          115
76 cac ccc cac cac gcg gtg aac act atc tcc acc cgg gtg gcg gct ggc      858
77 His Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala Ala Gly
78          120          125          130
80 atc gtc tgc acc ctg tgg gcc ctg gtc atc ctg gga aca gtg tat ctt      906
81 Ile Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val Tyr Leu
82 135          140          145          150
84 ttg ctg gag aac cat ctc tgc gtg caa gag acg gcc gtc tcc tgt gag      954
85 Leu Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser Cys Glu
86          155          160          165
88 agc ttc atc atg gag tcg gcc aat ggc tgg cat gac atc atg ttc cag      1002
89 Ser Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met Phe Gln
90          170          175          180
92 ctg gag ttc ttt atg ccc ctc ggc atc atc tta ttt tgc tcc ttc aag      1050
93 Leu Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser Phe Lys
94          185          190          195
96 att gtt tgg agc ctg agg cgg agg cag cag ctg gcc aga cag gct cgg      1098
97 Ile Val Trp Ser Leu Arg Arg Arg Gln Gln Leu Ala Arg Gln Ala Arg
98          200          205          210
100 atg aag aag gcg acc cgg ttc atc atg gtg gtg gca att gtg ttc atc      1146
101 Met Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val Phe Ile
102 215          220          225          230
104 aca tgc tac ctg ccc agc gtg tct gct aga ctc tat ttc ctc tgg acg      1194
105 Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu Trp Thr
106          235          240          245
108 gtg ccc tcg agt gcc tgc gat ccc tct gtc cat ggg gcc ctg cac ata      1242
109 Val Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu His Ile
110          250          255          260
112 acc ctc agc ttc acc tac atg aac agc atg ctg gat ccc ctg gtg tat      1290
113 Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu Val Tyr
114          265          270          275
116 tat ttt tca agc ccc tcc ttt ccc aaa ttc tac aac aag ctc aaa atc      1338
117 Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu Lys Ile
118          280          285          290
120 tgc agt ctg aaa ccc aag cag cca gga cac tca aaa aca caa agg ccg      1386
121 Cys Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln Arg Pro
122 295          300          305          310
124 gaa gag atg cca att tcg aac ctc ggt cgc agg agt tgc atc agt gtg      1434
125 Glu Glu Met Pro Ile Ser Asn Leu Gly Arg Arg Ser Cys Ile Ser Val
126          315          320          325
128 gca aaa gtt tcc aaa gcc agt ctg atg ggc aat ggg atc ccc act tgt      1482
129 Ala Lys Val Ser Lys Ala Ser Leu Met Gly Asn Gly Ile Pro Thr Cys

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130          330          335          340
132 tgagtggcac tgaacaagca gaccaacaac actgaggaag atagagtggg gacttagaat 1542
134 taactcgtgc taaggggtcg ggggctttga aaatgccacc cccctttctt attgcaagac 1602
136 ggcttctcgc acatgaactg catccttctc attctgtcgg aaatgaaatt cacacaacta 1662
138 taccttttgg ggaggttcca gttgattgaa gtgagttggc tgcattttct tatctgatca 1722
140 caatggcagg ggacagaatg tgcattggag ggagcatgtg tgtgttggga ggggggctag 1782
142 gaactgcaca gcccttgtgt aattttcgtt gtttgttttt gttttgagac agagtctcac 1842
144 tctgtgtccc aggttgagg gacgtggcac agtctcggct cactgcaacc tctgcctccc 1902
146 gggttcaagc aattctcctg cctcagcctc ccgagtagct gggattagag gcgccagcca 1962
148 acacaccggg ctaatttttg tatttttagt agagacaggg ttttgccatg ttggccaggc 2022
150 tgggtctcgc ctcttgacct caggtgatcc gcctgccttg gcctcccaaa gtgggtggat 2082
152 cacaggcgtg agccaccgtg cccggcctcc cctgtgtcat tttaaatggc taagtaaattg 2142
154 ggtatatgtg tttgaatggg gcatgttcac tctcttaggg gctatggggc agtttagcagc 2202
156 atttctctat ctctgacctt aaatcattcc ttatctcaga aaacagaaac cgggctcagt 2262
158 caatcaatgc tttattttcag gccgaatgag gctctttaga ttgggatcta ttgatctatc 2322
160 aattttcctc tttacatttc tttgtacatc tgtacatttt gtccaaatgt acatctgtac 2382
162 gtctgtcatc attgtgactt cctggtagcc caagaagaac aacaacaaaa caatctgtct 2442
164 tgaccttctt caaatctttg tatttcaaag aaggtgctga gggatctgtt tccttgccct 2502
166 ggcttctcca gtgggatgtg ctgagtccaa tacaattgct tttataattg cttttgaaaa 2562
168 aaaaaaaaaa aaaaaaag 2580
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 342
173 <212> TYPE: PRT
174 <213> ORGANISM: homo sapiens
176 <400> SEQUENCE: 2
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179 1          5          10          15
182 Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
183          20          25          30
186 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
187          35          40          45
190 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
191          50          55          60
194 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
195 65          70          75          80
198 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
199          85          90          95
202 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
203          100          105          110
206 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
207          115          120          125
210 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
211          130          135          140
214 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
215 145          150          155          160
218 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
219          165          170          175
222 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
223          180          185          190

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226 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
227      195      200      205
230 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
231      210      215      220
234 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
235 225      230      235      240
238 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
239      245      250      255
242 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
243      260      265      270
246 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
247      275      280      285
250 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
251      290      295      300
254 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
255 305      310      315      320
258 Arg Ser Cys Ile Ser Val Ala Lys Val Ser Lys Ala Ser Leu Met Gly
259      325      330      335
262 Asn Gly Ile Pro Thr Cys
263      340
266 <210> SEQ ID NO: 3
267 <211> LENGTH: 362
268 <212> TYPE: PRT
269 <213> ORGANISM: GALLUS GALLUS
271 <400> SEQUENCE: 3
273 Met Thr Glu Ala Leu Ile Ser Ala Ala Leu Asn Gly Thr Gln Pro Glu
274 1      5      10      15
276 Leu Leu Ala Gly Gly Trp Ala Ala Gly Asn Ala Thr Thr Lys Cys Ser
277      20      25      30
279 Leu Thr Lys Thr Gly Phe Gln Phe Tyr Tyr Leu Pro Thr Val Tyr Ile
280      35      40      45
282 Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met
283      50      55      60
285 Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe
286 65      70      75      80
288 Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu
289      85      90      95
291 Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met
292      100      105      110
294 Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile
295      115      120      125
297 Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His
298      130      135      140
300 Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val
301 145      150      155      160
303 Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu
304      165      170      175
306 Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr
307      180      185      190

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309 Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met
310      195      200      205
312 Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly
313      210      215      220
315 Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn
316 225      230      235      240
318 Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr
319      245      250      255
321 Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn
322      260      265      270
324 Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn
325      275      280      285
327 Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu
328      290      295      300
330 Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe
331 305      310      315      320
333 Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu
334      325      330      335
336 Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr
337      340      345      350
339 Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu
340      355      360
342 <210> SEQ ID NO: 4
343 <211> LENGTH: 362
344 <212> TYPE: PRT
345 <213> ORGANISM: MELEAGRIS GALLOPAVO
347 <400> SEQUENCE: 4
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350 1      5      10      15
352 Leu Leu Ala Gly Gly Trp Ala Ala Gly Asn Ala Ser Thr Lys Cys Ser
353      20      25      30
355 Leu Thr Lys Thr Gly Phe Gln Phe Tyr Tyr Leu Pro Thr Val Tyr Ile
356      35      40      45
358 Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met
359      50      55      60
361 Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe
362 65      70      75      80
364 Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu
365      85      90      95
367 Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met
368      100      105      110
370 Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile
371      115      120      125
373 Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His
374      130      135      140
376 Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val
377 145      150      155      160
379 Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu
380      165      170      175

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/092,135

DATE: 03/26/2002

TIME: 12:33:43

Input Set : A:\EP.txt

Output Set: N:\CRF3\03262002\J092135.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date